EXHIBIT D:

COMPARISON OF RAT AND HUMAN LKB1

BLAST

Basic Local Alignment Search Tool

-

Blast 2 sequences

SEQ ID NO: 6

Results for: | lcl|17777 SEQ ID NO: 6(433aa) ▾|
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to
show BLAST results for.

Query ID
lcl|17777
lcl|17777
Description
SEQ ID NO: 6
Molecule type
amino acid
Query Length
433

Subject ID
gi|157820995|ref|NP_001101539.1|
Description
serine/threonine-protein kinase 11 [Rattus norvegicus] >gi|149034596|gb|EDL89333.1| serine/threonine
kinase 11 (predicted), isoform CRA_a [Rattus norvegicus]
Molecule type
amino acid
Subject Length
436
Program
BLASTP 2.2.24+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller,
and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A.
Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution
matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Multiple alignment]
Search Parameters

Search parameter name Search parameter value

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62

Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.320459	0.267
K	0.139595	0.041
H	0.429592	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

Effective search space	110297

Graphic Summary

Distribution of Blast Hits on the Query Sequence

[?] _____

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

<u>Dot Matrix View</u>

Plot of lcl|17777 vs gi|157820995|ref|NP_001101539.1| [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is
represented on the X-axis and the numbers represent the bases/residues of the query. The subject is
represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are
shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right
corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in
the plot is the same as the number of alignments found by BLAST.

$$\boxed{\times}$$

Descriptions

	Score	E
	(Bits)	Value

Sequences producing significant alignments:

<u>ref|NP_001101539.1|</u>   serine/threonine-protein kinase 11 [Rattu...   <u>525</u>   1e-153

Alignments

```
>ref|NP_001101539.1| serine/threonine-protein kinase 11 [Rattus norvegicus]
 gb|EDL89333.1| serine/threonine kinase 11 (predicted), isoform CRA_a [Rattus
norvegicus]
Length=436

 Score =  525 bits (1351),  Expect = 1e-153, Method: Compositional matrix adjust.
 Identities = 287/300 (96%), Positives = 291/300 (97%), Gaps = 0/300 (0%)

Query  44    KLIGKYLMGDLLGEGSYGKVKEVLDSETLCRRAVkilkkklrriPNGEANVKKEIQLLR   103
             KLIGKYLMGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKLRRIPNGEANVKKEIQLLR
Sbjct  44    KLIGKYLMGDLLGEGSYGKVKEVLDSETLCRRAVKILKKKLRRIPNGEANVKKEIQLLR   103

Query  104   RLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPVCQAHGYFCQLIDG   163
             RLRH+NVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPVCQAHGYF QLIDG
Sbjct  104   RLRHRNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPVCQAHGYFRQLIDG   163

Query  164   LEYLHSQGIVHKDIKPgnlllttggtlKISDLGVAEALHPFAADDTCRTSQGSPAFQPPE   223
             LEYLHSQGIVHKDIKPGNLLLTT GTLKISDLGVAEALHPFA DDTCRTSQGSPAFQPPE
Sbjct  164   LEYLHSQGIVHKDIKPGNLLLTTNGTLKISDLGVAEALHPFAVDDTCRTSQGSPAFQPPE   223

Query  224   IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGKGSYAIPGDCGPPLS   283
             IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIG+G + IP DC PPLS
Sbjct  224   IANGLDTFSGFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGRGDFTIPCDCAPPLS   283

Query  284   DLLKGMLEYEPAKRFSIRQIRQHSWFRKKHppaeapvpippsPDTKDRWRSMTVVPYLED   343
             DLL+GMLEYEPAKRFSIRQIRQHSWFRKHP AEA VPIPPSPDTKDRWRSMTVVPYLED
Sbjct  284   DLLRGMLEYEPAKRFSIRQIRQHSWFRKKHPLAEALVPIPPSPDTKDRWRSMTVVPYLED   343
```